



129321.6.ST25.txt  
SEQUENCE LISTING

<110> Ramot University Authority for Applied Research & Industrial  
Development Ltd.

<120> A METHOD AND SYSTEM FOR PREDICTING AMINO ACID SEQUENCES  
COMPATIBLE WITH A SPECIFIED THREE DIMENSIONAL STRUCTURE

<130> 129321.6

<140> 09/718,425

<141> 2000-11-24

<150> IL 137886

<151> 2000-08-16

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 28

<212> PRT

<213> Unknown

<220>

<223> Zif268 wild-type suquence

<400> 1

Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp  
1 5 10 15

His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu  
20 25

<210> 2

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> FSD-1 - the sequence as designed by D&M. [Dahiyat BB.I. & Mayo  
S.

I. Protein Sci. 5::895-903 (1997)]

129321.6.ST25.txt

<400> 2

Gln Gln Tyr Thr Ala Lys Ile Lys Gly Arg Thr Phe Arg Asn Glu Lys  
1 5 10 15

Glu Leu Arg Asp Phe Ile Glu Lys Phe Lys Gly Arg  
20 25

<210> 3

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence obtained by the present invention using solvent  
accessibility (SA) calculation

<400> 3

Glu His Met Phe Val His His His Thr Thr Arg Phe Ser Ser His Thr  
1 5 10 15

Ser Phe Thr Ser Phe Leu Arg Ser Met Gln Gly Arg  
20 25

<210> 4

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence obtained by the present invention using D&M (Dahiyat  
BB.

I. & Mayo S.I. Protein Sci. 5::895-903 (1997) ) solvent  
accessibility (SA) fitted assignments

<400> 4

Gln His Met Thr Val His Phe His Asn Thr Thr Phe Ser His His Ser  
1 5 10 15

129321.6.ST25.txt

Ser Leu Ser Thr Phe Leu Gln Ser Phe Gln Gly Arg  
20 25

<210> 5  
<211> 8  
<212> PRT  
<213> Unknown

<220>  
<223> Streptococcal protein G derived from a larger multi-domain cell  
s  
urface protein that functions with high affinity binding to the  
F  
c region of IgG

<400> 5

Tyr Leu Thr Thr Thr Val Val Trp  
1 5

<210> 6  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> mutated residues in the lowest energy sequences kept in their  
na  
tive rotameric conformation

<400> 6

Leu Leu Leu Phe Leu Leu Val Met  
1 5

<210> 7  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> mutated residues in the lowest energy sequences in which  
rotamer  
ic states of the side chains of the non-mutating residues were  
al

129321.6.ST25.txt

lowed to change

<400> 7

Leu Leu Phe Leu Leu Ser Val Phe  
1 5

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence designated by M&M. Nat.Struc. Biol. 5:470-475 (1998)

<400> 8

Phe Ile Ile Ile Gln Ile Ile Ile  
1 5